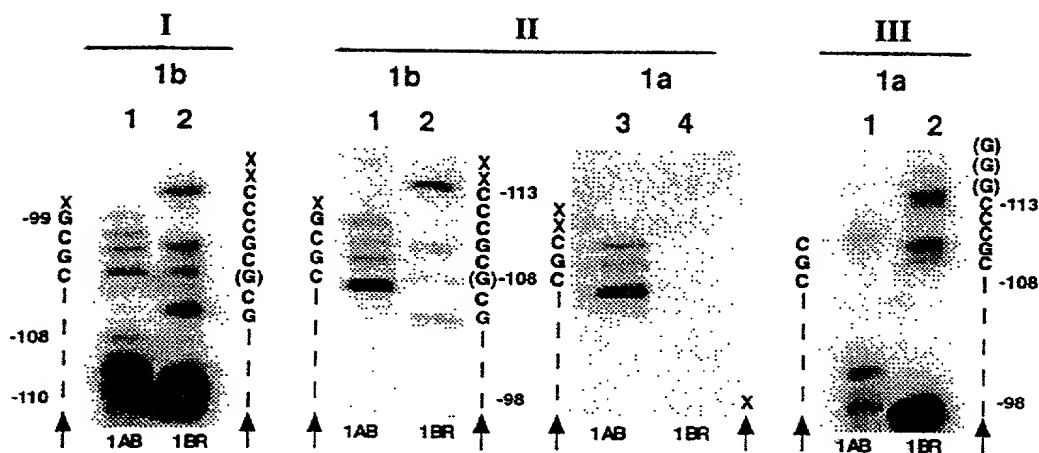


1/10



-113    -108                    -99

1a 5'-----TTTGGGCG (T) GCGGGGCGAAGAC-----3'

X← 1BR 5'

1b 5'-----TTTGGGCG (T) GCGGGGCGAGAC-----3'

XXXCCCGC (G) CGGGGGCGC← 1BR 5'

I' and II'

1a 3'-----AAACCCGC (A) CGGGGGCGTTCTG-----5'

5' 1AB CG (C) GCGGGGCGXX

1b 3'-----AAACCCGC (A) CGGGGGCGCTCTG-----5'

5' 1AB CG (C) GCGGGGCGX X

III'

-113    -108                    -99

1a 5'-----TTTGGGCG (T) GCGGGGCG (A) AGAC-----3'

AAACCCGC (G) CGGGGGCG (C) ← 1BR 5'

Figure 1

PRIMER-SPECIFIC AND MISPAIR EXTENSION  
ASSAY FOR IDENTIFYING GENE VARIATION

Yu-Wen Hu

Serial No. 09/782,361

Filed February 13, 2001

2/10

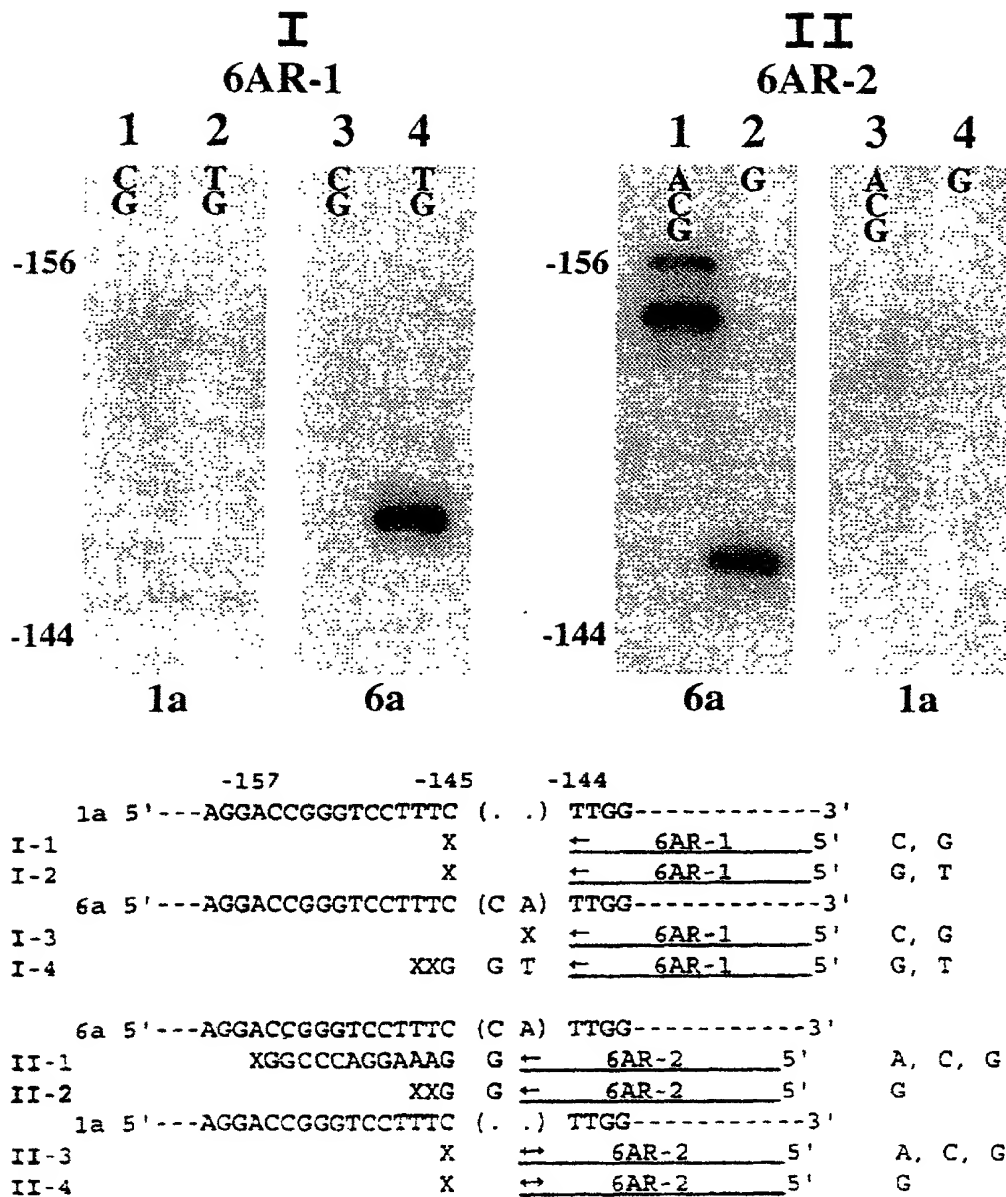


FIG. 2

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3/10

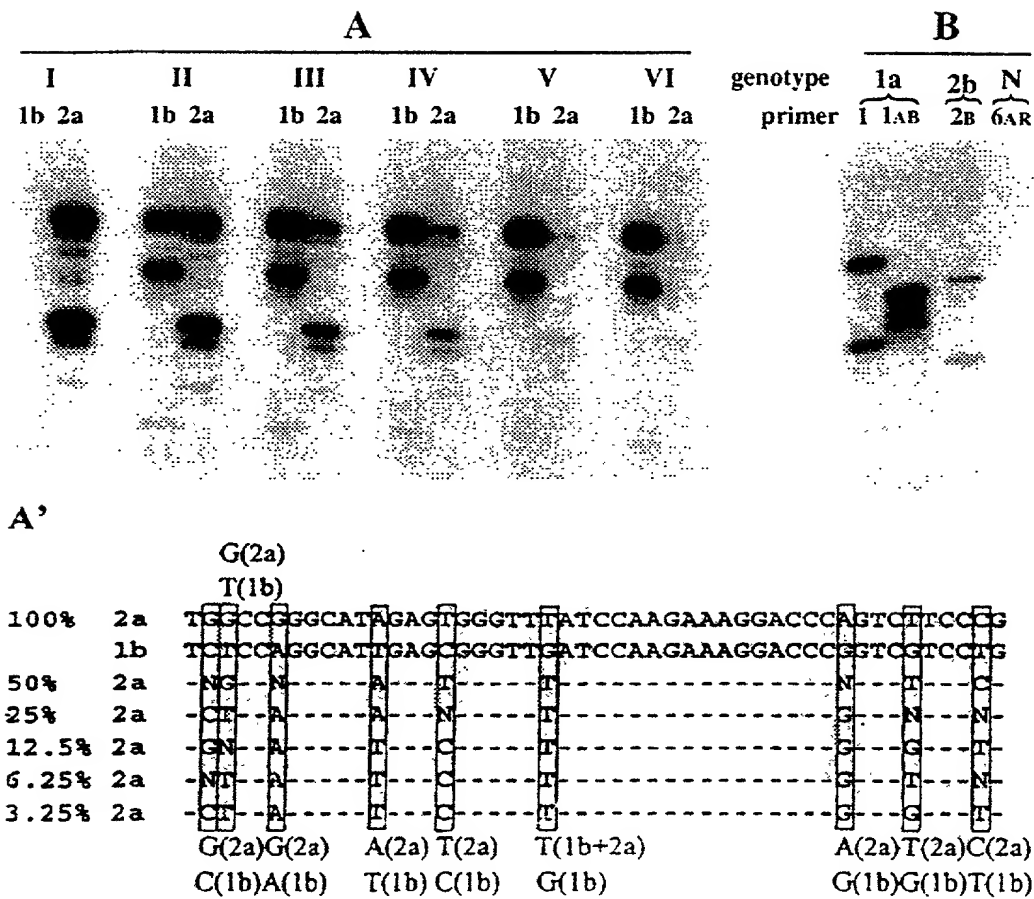


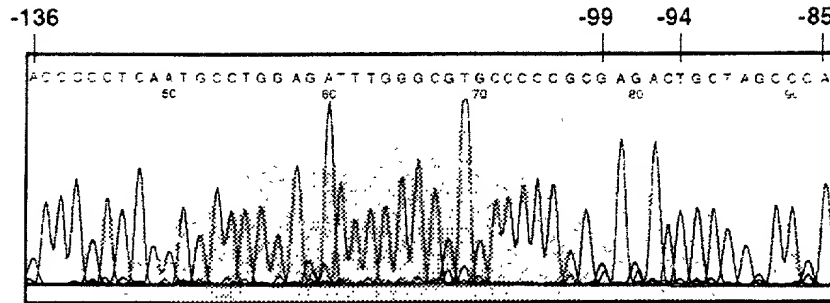
FIG. 3

PRIMER-SPECIFIC AND MISPAIR EXTENSION  
ASSAY FOR IDENTIFYING GENE VARIATION

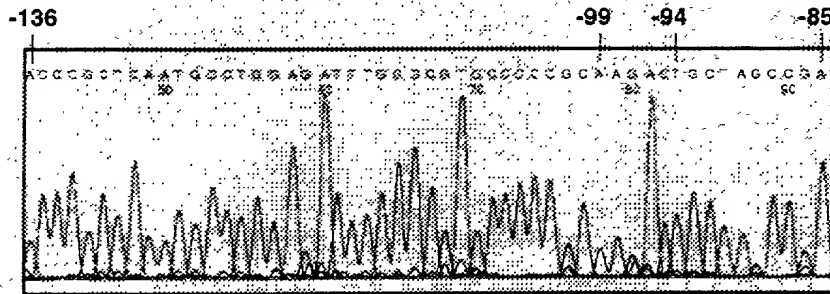
Yu-Wen Hu  
Serial No. 09/782,361  
Filed February 13, 2001

4/10

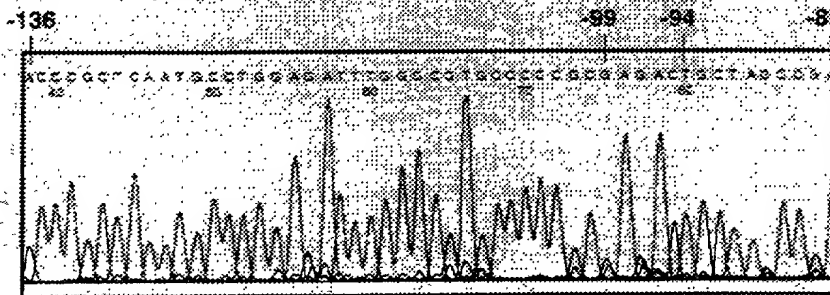
I J  
(1b)



H  
(1a)



I  
(1b)



II

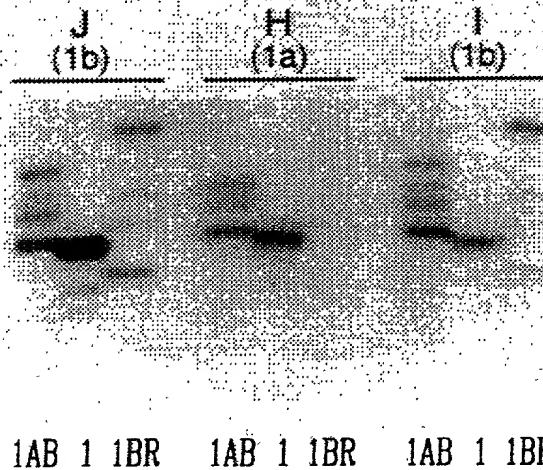


FIG. 4

FEES

782,361

3' **XTCATAC**TAXTCCATGAGTATCTTTAGACACCTGTATTTCG 5' L63 + PRIMER (1) (SEQ ID NO:18)  
5' AGACAGTATGATCAGGTACTCATAGAAATCTGTGGACATAAAGC 3' PRO63L(G)-R (SEQ ID NO:19)

**X**

3' GAGTATCTTTAGACACCTGTATTTCG 5' L63P + PRIMER (2) (SEQ ID NO:20)  
5' AGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAAGC 3' PRO63L(G)-R (SEQ ID NO:21)

6/10

3' **XTCATAC**TAXTCCATGGGTATCTTTAGACACCTGTATTTCG 5' L63P + PRIMER (3) (SEQ ID NO:22)  
5' AGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAAGC 3' PRO63P(G)-R (SEQ ID NO:21)

**X**

3' GGGTATCTTTAGACACCTGTATTTCG 5' L63 + PRIMER (4) (SEQ ID NO:23)  
5' AGACAGTATGATCAGGTACTCATAGAAATCTGTGGACATAAAGC 3' PRO63P(G)-R (SEQ ID NO:19)

782,361 - BA

PRIMER-SPECIFIC AND MISPAIR EXTENSION  
ASSAY FOR IDENTIFYING GENE VARIATION

Yu-Wen Hu

Serial No. 09/782,361

Filed February 13, 2001

7/10

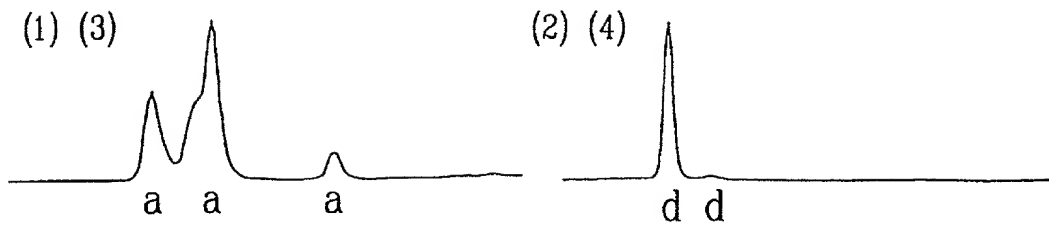


FIG. 1

5' CTGTCAACATAATTGGAAGAAATCTGAT 3' PRO90M-F (4) (SEQ ID NO:30)  
3' --GACAGTTGTATTAACTTCTTTAGACAACTGAGTCTAA--5' L90 (SEQ ID NO:31)

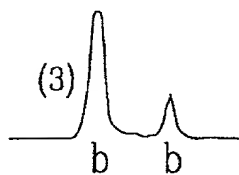
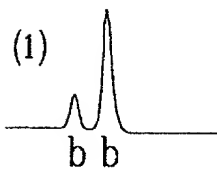
PRIMER-SPECIFIC AND MISPAIR EXTENSION  
ASSAY FOR IDENTIFYING GENE VARIATION

Yu-Wen Hu

Serial No. 09/782,361

Filed February 13, 2001

9/10

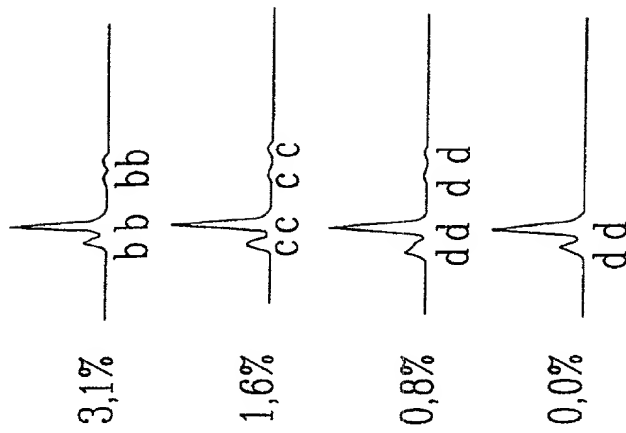


FE-7B

PRIMER-SPECIFIC AND MISPAIR EXTENSION  
ASSAY FOR IDENTIFYING GENE VARIATION

Yu-Wen Hu  
Serial No. 09/782,361  
Filed February 13, 2001

10/10



MU → T AGTTGTATTAAXX (SEQ ID NO: 32)  
----- A TCAACATAATTGGAAGA (SEQ ID NO: 33)

→ X  
----- G -----

FIG. 10